IN THE CLAIMS:

Please cancel claims 13, 14, 24, 33 and 37 without prejudice to or disclaimer of the subject matter contained therein.

Please replace claims 1-10, 18, 25-32, 34 and 35 as follows:

1. (Twice Amended) A nucleic material of the retroviral genomic type, in an isolated or purified state, comprising a reference nucleotide sequence selected from the group consisting of sequences of SEQ ID NOs: 1 to 15, their complementary sequences, and sequences that exhibit for every sequence of 100 contiguous monomers at least 70% homology with said sequences of SEQ ID NOs: 1 to 15, respectively.

2. (Twice Amended) A nucleic material of the retroviral genomic type, in an isolated or purified state, comprising a reference nucleotide sequence, encoding any polypeptide exhibiting, for every contiguous sequence of at least 30 amino acids, at least 80% identity with a peptide sequence encoded by at least a functional part of a reference nucleotide sequence selected from the group consisting of sequences of SEQ ID NOs: 1 to 15 and their complementary sequences.

3. (Three Times Amended) The nucleic material of the retroviral genomic type according to claim 1, comprising a nucleic fragment inserted between two sequences corresponding respectively to the LTR region and to the gag gene for the retroviral genomic structure.

4. (Twice Amended) A nucleic material of the subgenomic retroviral type, consisting of a nucleotide sequence identical to SEQ ID NO: 11, with at least one deletion.

5. (Twice Amended) A nucleic material according to claim 1, comprising at least one functional nucleotide sequence encoding at least one retroviral protein.

6. (Twice Amended) A nucleic material according to claim 1, comprising at least one regulatory nucleotide sequence.

7. (Three Times Amended) A nucleotide fragment comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence of at least 100 bases of a clone selected from the group consisting of:

cl.6A2 (SEQ ID NO: 1),

cl.6A1 (SEQ ID NO: 2),

cl.7A16 (SEQ ID NO: 3),

cl.Pi22 (SEQ ID NO: 4),

cl.24.4 (SEQ ID NO: 5),

cl.C4C5 (SEQ ID NO: 6),

cl.PH74 (SEQ ID NO: 7),

cl.PH7 (SEQ ID NO: 8),

cl.Pi5T (SEQ ID NO: 9),

cl.44.4 (SEQ ID NO: 10),

HERV-W (SEQ ID NO: 11),

cl.6A5 (SEQ ID NO: 12),

cl.7A20 (SEQ ID NO: 13),

cl.7A21 (SEQ ID NO: 14), and

LTR (SEQ ID NO: 15);

(b) sequences which are respectively complementary to the sequences according to (a); and

(c) equivalent sequences which have respectively at least 50% homology to the sequences according to (a) and (b).

8. (Three Times Amended) A nucleic probe for the detection of a nucleic material, wherein said nucleic probe hybridizes under highly stringent conditions with the reference nucleotide sequence of the nucleic material according to claim 1.

D1 cont

9. (Twice Amended) A probe according to claim 8, comprising a label.

10. (Three Times Amended) A nucleic primer for the amplification by polymerization of an RNA or of a DNA, comprising a nucleotide sequence that hybridizes under highly stringent conditions with the reference nucleotide sequence of the nucleic material according to claim 1.

18. (Twice Amended) A method for the molecular labeling of at least one member selected from the group consisting of an autoimmune disease, a pathology associated with an autoimmune disease, a pathological pregnancy, and an unsuccessful pregnancy, said method comprising:

D2

at least one of identifying and quantifying any nucleotide fragment according to claim 7 in any biological body material.

25. (Amended) The nucleic material according to claim 1, wherein said reference nucleotide sequence exhibits, for every sequence of 100 contiguous monomers, at least 90% homology with said sequences of SEQ ID NOs: 1 to 15, respectively.

26. (Amended) The nucleic material according to claim 2, wherein said polypeptide exhibits, for every contiguous sequence of at least 30 amino acids, at least 90% identity with a peptide sequence capable of being encoded by at least a functional part of said reference nucleotide sequence.

D3

27. (Amended) The nucleic material of the retroviral genomic type according to claim 2, comprising a nucleic fragment inserted between two sequences corresponding respectively to the LTR region and to the gag gene for said retroviral genomic structure.

28. (Amended) The nucleic material according to claim 27, wherein said nucleic fragment comprises the sequence of SEQ ID NO: 12.

29. (Amended) The nucleic material according to claim 3, wherein said nucleic fragment comprises the sequence of SEQ ID NO: 12.

D3 cont

30. (Amended) The nucleic material according to claim 4, wherein said nucleotide sequence comprises a sequence selected from the group consisting of the sequences of SEQ ID NOs: 7, 8 and 9.

31. (Amended) The nucleic material according to claim 4, comprising at least one functional nucleotide sequence encoding at least one retroviral protein.

32. (Amended) The nucleic material according to claim 4, comprising at least one regulatory nucleotide sequence.

34. (Amended) A nucleotide fragment according to claim 7, wherein said equivalent sequences exhibit at least 70% homology with the sequences according to (a) and (b).

D4

35. (Amended) A nucleotide fragment according to claim 7, wherein said equivalent sequences exhibit at least 90% homology with the sequences according to (a) and (b).

Please add new claims 39-48 as follows:

--39. The nucleic probe according to claim 8, wherein said probe contains at least 6 monomers.--

--40. The nucleic probe according to claim 39, wherein said probe contains no more than 100 monomers.--

D5

--41. The nucleic probe according to claim 39, wherein said probe contains at least 6 contiguous monomers of a sequence selected from the group consisting of SEQ ID NOs: 1-15 and their complementary sequences.--

--42. The nucleic probe according to claim 8, wherein said probe has at least 70% homology with a sequence selected from the group consisting of SEQ ID NOs: 1-15 and their complementary sequences.--

--43. The nucleic probe according to claim 42, wherein said probe has at least 90% homology with a sequence selected from the group consisting of SEQ ID NOs: 1-15 and their complementary sequences.--

--44. The nucleic primer according to claim 10, wherein said primer contains at least 6 monomers.--

DS cont

--45. The nucleic primer according to claim 44, wherein said primer contains no more than 30 monomers.--

--46. The nucleic primer according to claim 44, wherein said primer contains at least 6 contiguous monomers of a sequence selected from the group consisting of SEQ ID NOs: 1-15 and their complementary sequences.--

--47. The nucleic primer according to claim 10, wherein said primer has at least 70% homology with a sequence selected from the group consisting of SEQ ID NOs: 1-15 and their complementary sequences.--

--48. The nucleic primer according to claim 47, wherein said primer has at least 90% homology with a sequence selected from the group consisting of SEQ ID NOs: 1-15 and their complementary sequences.--